

1/13

SEQUENCE LISTING

<110> KANEKA CORPORATION

<120> NOVEL ACYLASE GENE

<130> T719. /ACYL-1

<150> JP P2002-165722

<151> 2002-06-06.

<160> 15

<210> 1

<211> 2529

<212> DNA

<213> Stenotrophomonas maltophilia

<220>

<221> CDS

<222> (126)... (2036)

<400> 1

tctacaacgg cttggcacat gtgccatcag tctaccccc aaagagcgca gaacgcaaag 60

cctgcacaca cttcacccgc cggggcagga gtacgcttgg gactttcctg cccgaggggt 120

cgtcc atg cat gtg cgt gcc gta gca gtt gcc atc gcc ctg agc ctg tcc 170

Met His Val Arg Ala Val Ala Val Ala Ile Ala Leu Ser Leu Ser

1

5

10

15

agc acc gtg ctg gcc gcc gac acc ccg ccg atg acc ccg gac atc agc 218

Ser Thr Val Leu Ala Ala Asp Thr Pro Pro Met Thr Pro Asp Ile Ser

20

25

30

ggc aag cct ttc att gcg ccc gat gtc ggc cgc gac tac gac aag cgc	266
Gly Lys Pro Phe Ile Ala Pro Asp Val Gly Arg Asp Tyr Asp Lys Arg	
35 40 45	
gtg gtg atg gtg ccg atg cgc gac ggt acc agg ctg tac acg gtg atc	314
Val Val Met Val Pro Met Arg Asp Gly Thr Arg Leu Tyr Thr Val Ile	
50 55 60	
gtg gtg ccc aag ggc gcg cac aat gcc ccg atc ctg ctg acc cgc acg	362
Val Val Pro Lys Gly Ala His Asn Ala Pro Ile Leu Leu Thr Arg Thr	
65 70 75	
ccc tac gat gct gcc ggc cgc gcc agc cgc agc gat tcg ccg cgc atg	410
Pro Tyr Asp Ala Ala Gly Arg Ala Ser Arg Ser Asp Ser Pro Arg Met	
80 85 90 95	
cgc gac ctg ctg ccg cag ggg gat gaa gtc ttc gtc gat ggc ggc tat	458
Arg Asp Leu Leu Pro Gln Gly Asp Glu Val Phe Val Asp Gly Gly Tyr	
100 105 110	
atc cgc gtg ttc cag gac atc cgg ggc aag tac ggt tcg gaa ggc gat	506
Ile Arg Val Phe Gln Asp Ile Arg Gly Lys Tyr Gly Ser Glu Gly Asp	
115 120 125	
tat gtg atg acc cgg ccg ctg cgc ggg ccg ttg aac aac acc aag gtc	554
Tyr Val Met Thr Arg Pro Leu Arg Gly Pro Leu Asn Asn Thr Lys Val	
130 135 140	
gac cac tcc acc gat gca tgg gac acc atc gac tgg ttg gtg aaa cac	602
Asp His Ser Thr Asp Ala Trp Asp Thr Ile Asp Trp Leu Val Lys His	
145 150 155	
gtg ccg gaa agc aac ggc aag gtc ggc atg ctg ggc tcg tcg tac gaa	650
Val Pro Glu Ser Asn Gly Lys Val Gly Met Leu Gly Ser Ser Tyr Glu	

160	165	170	175	
ggc ttc acc gtg gtg atg gcc ctg acc gac ccg cat ccg gcg ctg aag				698
Gly Phe Thr Val Val Met Ala Leu Thr Asp Pro His Pro Ala Leu Lys				
	180	185	190	
gtg gcc gcc ccg cag agc ccg atg gtc gat gcc tgg atg gcc gac gac				746
Val Ala Ala Pro Gln Ser Pro Met Val Asp Gly Trp Met Gly Asp Asp				
	195	200	205	
tgg ctc aac tac ggg gcc ttc cgc cag gtc aat ttc aac tac ttc gca				794
Trp Leu Asn Tyr Gly Ala Phe Arg Gln Val Asn Phe Asn Tyr Phe Ala				
	210	215	220	
atg cag acc gag aag cgc gcc aag gcc acg ccg ctg ccc agc ctg gcc				842
Met Gln Thr Glu Lys Arg Gly Lys Gly Thr Pro Leu Pro Ser Leu Gly				
	225	230	235	
tac gac gac tac agc acc ttc ctg cgc atc ggt tgc gcc ggt gac tac				890
Tyr Asp Asp Tyr Ser Thr Phe Leu Arg Ile Gly Ser Ala Gly Asp Tyr				
	240	245	250	255
gca cgc ttc acc gcc gtg gac cag ctg acc tgg tgg aag aag ctg gtg				938
Ala Arg Phe Thr Gly Val Asp Gln Leu Thr Trp Trp Lys Lys Leu Val				
	260	265	270	
cag cac ccg gcc tac gat gcc ttc tgg cag gcc cag gcg ctg gat gcg				986
Gln His Pro Ala Tyr Asp Gly Phe Trp Gln Gly Gln Ala Leu Asp Ala				
	275	280	285	
gtg atg gcg aag acc ccg ctg aag gtg ccg acc atg tgg ctg cag gcc				1034
Val Met Ala Lys Thr Pro Leu Lys Val Pro Thr Met Trp Leu Gln Gly				
	290	295	300	
ctg tgg gac cag gaa gac atg tgg gcc gcc aac cat gcc tac cag gcg				1082

Leu Trp Asp Gln Glu Asp Met Trp Gly Ala Asn His Ala Tyr Gln Ala	
305	310 315
atg gaa ggc cgc gac acc ggc aat acc cac aat tac ctg gtg atg ggc	1130
Met Glu Gly Arg Asp Thr Gly Asn Thr His Asn Tyr Leu Val Met Gly	
320	325 330 335
ccg tgg cgg cac agc cag gtg aac tac acc ggc aac gag ctg ggt gcg	1178
Pro Trp Arg His Ser Gln Val Asn Tyr Thr Gly Asn Glu Leu Gly Ala	
	340 345 350
ctg aag ttc gag ggc gat acc gcg ctg cag ttc cgc cgc gat gtg ctc	1226
Leu Lys Phe Glu Gly Asp Thr Ala Leu Gln Phe Arg Arg Asp Val Leu	
	355 360 365
aag ccg ttc ttc gac cag tac ctg gtg gat ggc gca ccg aag gcc gac	1274
Lys Pro Phe Phe Asp Gln Tyr Leu Val Asp Gly Ala Pro Lys Ala Asp	
	370 375 380
acg ccg ccg gtg ctc atc tac aac acc ggc gaa aac cac tgg gat cgc	1322
Thr Pro Pro Val Leu Ile Tyr Asn Thr Gly Glu Asn His Trp Asp Arg	
	385 390 395
ctg cag ggc tgg ccg cgc agt tgc gac aag ggc tgc acg gcg gcc agc	1370
Leu Gln Gly Trp Pro Arg Ser Cys Asp Lys Gly Cys Thr Ala Ala Ser	
400	405 410 415
aag ccg ctg tac ctg cgt gcc ggt ggc aag ctg gcc ttc cag gca ccg	1418
Lys Pro Leu Tyr Leu Arg Ala Gly Gly Lys Leu Ala Phe Gln Ala Pro	
	420 425 430
gcg gcg ggt gaa ggt gat ttc gag gaa tac gtg tcc gac ccg gcc aag	1466
Ala Ala Gly Glu Gly Asp Phe Glu Glu Tyr Val Ser Asp Pro Ala Lys	
	435 440 445

ccg gtg ccg ttc gtg ccg cgc ccg gtg cgt ttt ggc gac cgt gac atg	1514
Pro Val Pro Phe Val Pro Arg Pro Val Arg Phe Gly Asp Arg Asp Met	
450 455 460	
tgg acc acg tgg ctg gtg aag gac caa cgt ttt gtc gat ggt cgt ccg	1562
Trp Thr Thr Trp Leu Val Lys Asp Gln Arg Phe Val Asp Gly Arg Pro	
465 470 475	
gat gtg ctg acc ttc atc acc gaa ccg ctg gcc gag ccg ctg cgg atc	1610
Asp Val Leu Thr Phe Ile Thr Glu Pro Leu Ala Glu Pro Leu Arg Ile	
480 485 490 495	
ggc ggc gcg ccg gtg gtg cat ctg cag gcg tcc acc agt ggc acc gac	1658
Gly Gly Ala Pro Val Val His Leu Gln Ala Ser Thr Ser Gly Thr Asp	
500 505 510	
agc gac tgg gtg gtg aag ctg atc gac gtc tac ccg gat cag gaa gcg	1706
Ser Asp Trp Val Val Lys Leu Ile Asp Val Tyr Pro Asp Gln Glu Ala	
515 520 525	
tca acg ccg gaa atg ggt ggc tat gag ctg ccg gtg tcg ctg gcg atc	1754
Ser Thr Pro Glu Met Gly Gly Tyr Glu Leu Pro Val Ser Leu Ala Ile	
530 535 540	
ttc cgt ggg cgc tat cgg gag agt ttc agc gac ccg aag ccg ctg gca	1802
Phe Arg Gly Arg Tyr Arg Glu Ser Phe Ser Asp Pro Lys Pro Leu Ala	
545 550 555	
gcg aac cag gtg ctg ccg tac cgc ttt gat ctg ccc aat gcc aac cat	1850
Ala Asn Gln Val Leu Pro Tyr Arg Phe Asp Leu Pro Asn Ala Asn His	
560 565 570 575	
gtg ttc cag aag ggg cac cgg gtg atg gtg cag gtg cag tcc agc ctg	1898
Val Phe Gln Lys Gly His Arg Val Met Val Gln Val Gln Ser Ser Leu	
580 585 590	

ttc ccg ctg tat gac cgc aac ccg cag acc tac gtg ccg aac atc tac 1946
Phe Pro Leu Tyr Asp Arg Asn Pro Gln Thr Tyr Val Pro Asn Ile Tyr
595 600 605

ctg gcc aag ccg ggc gat tac cag aag gcc acg cag cgg gtg tgg cac 1994
Leu Ala Lys Pro Gly Asp Tyr Gln Lys Ala Thr Gln Arg Val Trp His
610 615 620

agc gcc gcg cag gcg agc tac gtc gac ctg ccg gtg tac tga 2036
Ser Ala Ala Gln Ala Ser Tyr Val Asp Leu Pro Val Tyr
625 630 635

ggcggagaat ggcgtggtag tgccggccgc tggccggcaa cgcggagcgg tagcgcggg 2096

ccatgcccg cggatggggt agtgccggcc gctggccggc aacgcggtga agccggcgcg 2156

tgtcgaccaa ggccgacacc tgccagagca cgtcagccta ccttcgaggg accggtgcgc 2216

cagcggctgg gaaccagacc gaagcgcttg cggaaggcgg cggcgaagtt gctgggggtgg 2276

cggtagccgg tggcgtccgc cgcctgttca acgctccagc cgtgttcgcg caggccgcgt 2336

tggcgtggt gcatgcgttg ttcgtgcagg tagtcgaaca ccgagcacc gtattgctgc 2396

acgaagtggc ggccgcagcga gctgggactc atgcaggcca gctggggccag ttccaccagg 2456

ctgtgggcgt ggctgggata gtcgtgcagg aagccccgca cgcgttcaat cgggccaagt 2516

tggccgcgcc aaa 2529

<210> 2

<211> 636

<212> PRT

<213> *Stenotrophomonas maltophilia*

<400> 2

Met	His	Val	Arg	Ala	Val	Ala	Val	Ala	Ile	Ala	Leu	Ser	Leu	Ser	Ser
1				5					10					15	
Thr	Val	Leu	Ala	Ala	Asp	Thr	Pro	Pro	Met	Thr	Pro	Asp	Ile	Ser	Gly
			20					25					30		
Lys	Pro	Phe	Ile	Ala	Pro	Asp	Val	Gly	Arg	Asp	Tyr	Asp	Lys	Arg	Val
		35					40					45			
Val	Met	Val	Pro	Met	Arg	Asp	Gly	Thr	Arg	Leu	Tyr	Thr	Val	Ile	Val
	50					55					60				
Val	Pro	Lys	Gly	Ala	His	Asn	Ala	Pro	Ile	Leu	Leu	Thr	Arg	Thr	Pro
65					70					75					80
Tyr	Asp	Ala	Ala	Gly	Arg	Ala	Ser	Arg	Ser	Asp	Ser	Pro	Arg	Met	Arg
				85					90					95	
Asp	Leu	Leu	Pro	Gln	Gly	Asp	Glu	Val	Phe	Val	Asp	Gly	Gly	Tyr	Ile
			100					105					110		
Arg	Val	Phe	Gln	Asp	Ile	Arg	Gly	Lys	Tyr	Gly	Ser	Glu	Gly	Asp	Tyr
		115					120					125			
Val	Met	Thr	Arg	Pro	Leu	Arg	Gly	Pro	Leu	Asn	Asn	Thr	Lys	Val	Asp
	130					135						140			
His	Ser	Thr	Asp	Ala	Trp	Asp	Thr	Ile	Asp	Trp	Leu	Val	Lys	His	Val
145					150					155					160
Pro	Glu	Ser	Asn	Gly	Lys	Val	Gly	Met	Leu	Gly	Ser	Ser	Tyr	Glu	Gly
				165					170					175	
Phe	Thr	Val	Val	Met	Ala	Leu	Thr	Asp	Pro	His	Pro	Ala	Leu	Lys	Val
			180					185					190		
Ala	Ala	Pro	Gln	Ser	Pro	Met	Val	Asp	Gly	Trp	Met	Gly	Asp	Asp	Trp
		195					200					205			
Leu	Asn	Tyr	Gly	Ala	Phe	Arg	Gln	Val	Asn	Phe	Asn	Tyr	Phe	Ala	Met
	210					215						220			
Gln	Thr	Glu	Lys	Arg	Gly	Lys	Gly	Thr	Pro	Leu	Pro	Ser	Leu	Gly	Tyr
225				230						235					240
Asp	Asp	Tyr	Ser	Thr	Phe	Leu	Arg	Ile	Gly	Ser	Ala	Gly	Asp	Tyr	Ala
				245					250					255	

Arg Phe Thr Gly Val Asp Gln Leu Thr Trp Trp Lys Lys Leu Val Gln			
	260	265	270
His Pro Ala Tyr Asp Gly Phe Trp Gln Gly Gln Ala Leu Asp Ala Val			
	275	280	285
Met Ala Lys Thr Pro Leu Lys Val Pro Thr Met Trp Leu Gln Gly Leu			
	290	295	300
Trp Asp Gln Glu Asp Met Trp Gly Ala Asn His Ala Tyr Gln Ala Met			
305		310	315 320
Glu Gly Arg Asp Thr Gly Asn Thr His Asn Tyr Leu Val Met Gly Pro			
	325	330	335
Trp Arg His Ser Gln Val Asn Tyr Thr Gly Asn Glu Leu Gly Ala Leu			
	340	345	350
Lys Phe Glu Gly Asp Thr Ala Leu Gln Phe Arg Arg Asp Val Leu Lys			
	355	360	365
Pro Phe Phe Asp Gln Tyr Leu Val Asp Gly Ala Pro Lys Ala Asp Thr			
	370	375	380
Pro Pro Val Leu Ile Tyr Asn Thr Gly Glu Asn His Trp Asp Arg Leu			
385		390	395 400
Gln Gly Trp Pro Arg Ser Cys Asp Lys Gly Cys Thr Ala Ala Ser Lys			
	405	410	415
Pro Leu Tyr Leu Arg Ala Gly Gly Lys Leu Ala Phe Gln Ala Pro Ala			
	420	425	430
Ala Gly Glu Gly Asp Phe Glu Glu Tyr Val Ser Asp Pro Ala Lys Pro			
	435	440	445
Val Pro Phe Val Pro Arg Pro Val Arg Phe Gly Asp Arg Asp Met Trp			
	450	455	460
Thr Thr Trp Leu Val Lys Asp Gln Arg Phe Val Asp Gly Arg Pro Asp			
465		470	475 480
Val Leu Thr Phe Ile Thr Glu Pro Leu Ala Glu Pro Leu Arg Ile Gly			
	485	490	495
Gly Ala Pro Val Val His Leu Gln Ala Ser Thr Ser Gly Thr Asp Ser			
	500	505	510
Asp Trp Val Val Lys Leu Ile Asp Val Tyr Pro Asp Gln Glu Ala Ser			
	515	520	525
Thr Pro Glu Met Gly Gly Tyr Glu Leu Pro Val Ser Leu Ala Ile Phe			

530		535		540
Arg Gly Arg Tyr Arg Glu Ser Phe Ser Asp Pro Lys Pro Leu Ala Ala				
545		550		555
Asn Gln Val Leu Pro Tyr Arg Phe Asp Leu Pro Asn Ala Asn His Val				
	565		570	
Phe Gln Lys Gly His Arg Val Met Val Gln Val Gln Ser Ser Leu Phe				
	580		585	
Pro Leu Tyr Asp Arg Asn Pro Gln Thr Tyr Val Pro Asn Ile Tyr Leu				
	595		600	
Ala Lys Pro Gly Asp Tyr Gln Lys Ala Thr Gln Arg Val Trp His Ser				
	610		615	
Ala Ala Gln Ala Ser Tyr Val Asp Leu Pro Val Tyr				
625		630		635

<210> 3

<211> 25

<212> PRT

<213> *Stenotrophomonas maltophilia*

<220>

<221> PEPTIDE

<222> (1)... (25)

<400> 3

Val Pro Thr Met Trp Leu Gln Gly Leu Trp Asp Gln Glu Asp Met Trp

1

5

10

15

Gly Ala Asn His Ala Tyr Gln Ala Met

20

25

<210> 4

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: K1 primer

<400> 4

tgggaycarg argayatgtg ggg

23

<210> 5

<211> 8

<212> PRT

<213> Stenotrophomonas maltophilia

<220>

<221> PEPTIDE

<222> (1)... (8)

<400> 5

Trp Asp Gln Glu Asp Met Trp Gly

1

5

<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: K-Nde I-4 primer

<400> 6

ggaattccat atgcatgtgc gtgccgtagc

30

<210> 7

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: K-BamH I-1 primer

<400> 7

cgcggatcct cagtacaccg gcaggtc

27

<210> 8

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: MT-197 primer

<400> 8

aaaaagcagg ctggcacgac aggtttcccg actgga

36

<210> 9

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: MT-198 primer

<400> 9

agaaagctgg gtggatcctc agtacaccgg caggtcga

38

<210> 10

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: attB1 primer

<400> 10

ggggacaagt ttgtacaaaa aagcaggct

29

<210> 11

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: attB2 primer

<400> 11

ggggaccact ttgtacaaga aagctgggt

29

<210> 12

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: MT-216 primer

<400> 12

cgctctaga agcgattcgc cgcgcatgcg cgacc

35

<210> 13

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: MT-219 primer

<400> 13

gcacaagctt cttccaccag gtcagctgg

29

<210> 14

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: MT-217 primer

<400> 14

tcgcttctag aggcgcggcc ggcagcatcg tagggc

36

<210> 15

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: MT-218 primer

<400> 15

ggaagaagct tgtgcagcac ccggcc

26